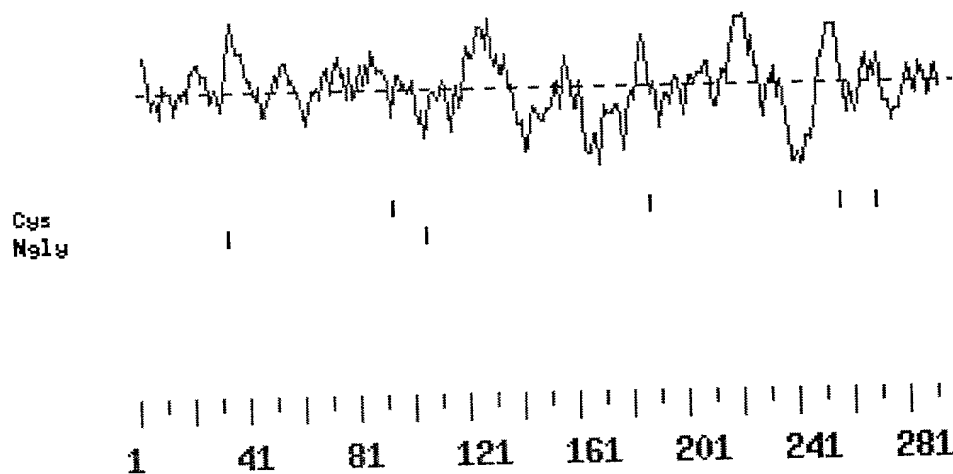


PFAM

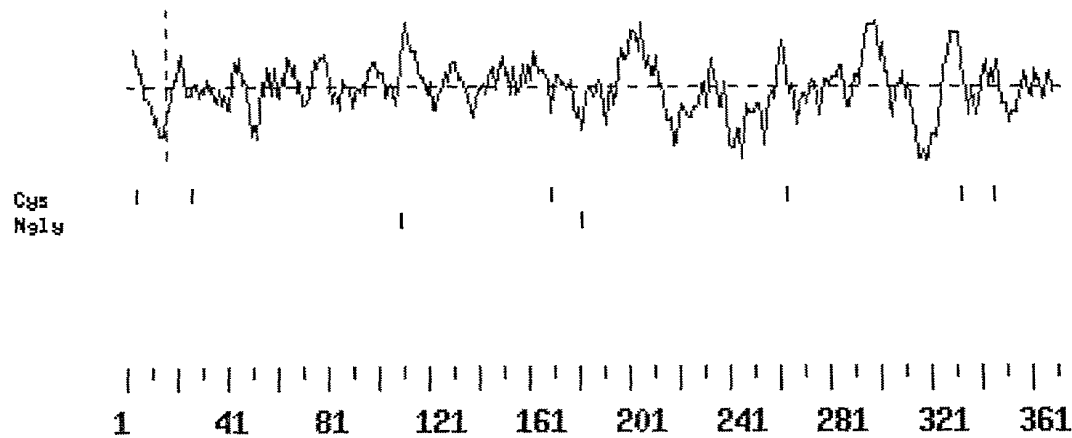


>8Apro

MLAAPINPSDINMIQGNYGLLPELPAVGGNEGVAQVVAVGSNVTGLKPGDWVIPANAGLG  
TWRTEAVFSEEALIQVPSDIPLOSAATLGVPNCTAYRMLMDFEQLQPGDSVIQNASNSGV  
GQAVIQIAAALGLRTINVVRDRPDIQKLSDRKSLGAEHVITEEELRRPEMKNFFKDMPQ  
PRLALNCVGGKSSTELLRQLARGGTMVTYGGMAKQPVVASVSLIFKDLKLRGFWLSQWK  
KDHSPDQFKELILTLCDLIRRGQLTAPACSQVPLQDYQSALEASMKPFISSKQILTM

FIGURE 1

PFAH



>8Bpro  
 MWVCSTLWRVRTPARQWRGLLPASGCHGPAASSYSASAEPARVRALVYGHGDPKVVVEL  
 KNLELAAVRGSDVRVKMLAAPINPSDINMIQGNYGLLPELPAVGGNEGVAQVAVGNSVT  
 GLKPGDWVIPANAGLGTWRTEAVFSEEALIQVPSDIPLOSAATLGVPCTAYRMLMDFEQ  
 LQPGDSVIQNASNSGVGQAVIQIAAALGLRTINVVRDRPDQKLSDRKSLGAEHVITEE  
 ELRRPEMKNEFFKDMPPRLALNCVGGKSSTELLRQLARGGTMVTYGGMAKQPVVASVSL  
 IFKDLKLRGFWSQWKDHSFDQFKELILTLCDLIRRGQLTAPACSQVPLQDYQSALEAS  
 MKPFISSKQILTM

FIGURE 2

adh\_zinc: domain 1 of 1, from 1 to 297: score 163.0, E = 5.2e-45  
 \*->pleveevvppepgpgeVlvkvkaaGiCgsDlhiykgglGlmypgpgd  
 1 aa i++sD+ +++g y+  
 8Apro 1 ML-----AAPINPSDINMIQGN---YGLL-- 21  
 gthlfpvklPlvlGHEgaGvVeeVGsgVtgfklkvkgfkvGDrVvvlplv  
 + lP v+G Eg+ +V++VGs+Vtg +k+GD V+++ +  
 8Apro 22 -----PELPAVGGNEGVAQVAVGSNVTG-----LKP GDWVIPANAG 58  
 gcCgrgsaeCefCkgsGrenlCpkgratgpgkGlm pndgfggftpkkgga  
 8Apro 59 L----- 59  
 PckGkdgyhfmgdGgfaEYvvvparrndyfvvkiPdgl ddeipleeeaaA  
 G++ + +v ++ ++ +P ++ pl A  
 8Apro 60 -----GTWRTEAVFSEE----ALIQVPSDI----PLQS---A 85  
 allgcaglTaygalvraakvgs lppGdtVlVhGaGGGVGlaAvqlAkaaG  
 a lg++ +Tay++l ++++ l+pGd+V + GVG+a++q+A a+G  
 8Apro 86 ATLG VNPCTAYRMLMDFEQ---LQPGDSVIQNASNSGVGQAVIQIAAALG 132  
 AarViavdssed. pekklelAkelGAdldadfvnnskglptvnddrkedf  
 +++ +v ++d ++ + l+ +lG a++v+ ++e  
 8Apro 133 LRTINVVRDPDiQKLS DRLK-SLG----AEHVIT-----EEELR 167  
 veaikeltgGrngagGvDvvldcvGiglggatldaalallkpgGrlvvvG  
 ++k +++ + + +l+c +gg++ ++l+ l++gG++v+ G  
 8Apro 168 RPEMKNFFKDM---PQPR LALNC---VGGKSSTELLRQLARGGTMV TYG 210  
 pkvavGvpvgggapipl..lllkeeklyersikGsflggrkprlsvlsvd  
 G++ ++ +++ l++k ++++G++l+++k +  
 8Apro 211 -----GMAKQPVVASVs lLIFKD-----LKL RGFWLSQWKKD----- 242  
 ttpdelreal d llasgikdkngkgvldplithtlpplddsleeaneA fel  
 ++pd ++e++ l ++i+ +g+l ++p l + + A+e+  
 8Apro 243 HSPDQFKELILTLCDLIR----RGQLTAPACSQVP-LQ----DYQSALEA 283  
 lesghk.gkvvlip<-\*  
 ++ ++ k++l++  
 8Apro 284 SMKPFIsSKQILTM 297

FIGURE 3

adh\_zinc: domain 1 of 1, from 57 to 373: score 212.3, E = 7.4e-60

```

      *->pleveevpvpepgpgeVlvkvkaaGiCgsDlhiykgglGlmypgpgd
            ++e++  +++  +  +V+vk+aa i++sD+  +++g      y+
8Bpro    57      VVELKNLELAAVRGSDVRVKMLAAPINPSDINMIQGN----YGLL-- 97

            gthlfpvklPlvlGHEgaGvVeeVGsgVtgfklkvvgkfkvGDrVvvlplv
            + 1P v+G Eg+ +V++VGs+Vtg      +k+GD V+++  +
8Bpro    98 -----PELPAVGGNEGVAQVVAVGSNVTG-----LKP GDWVIPANAG 134

            gcCgrgsaeCefCkgsGrenlCpkgratgpgkGlm pndgfggftpkkqga

8Bpro    135 L----- 135

            PckGkdgyhfmgdGgfaEYvvvparrndyfvvkiPdgl ddeipleeaeaA
            G++ + +v ++      ++ +P ++      pl      A
8Bpro    136 -----GTWRTEAVFSEE-----ALIQVPSDI-----PLQS---A 161

            allgcaglTaygalvraakvgs lppGdtVlVhGaGGGVGlaAvqlAkaaG
            a lg++ +Tay++l +++++  l+pGd+V  +  GVG+a++q+A a+G

8Bpro    162 ATLG VNPCTAYRMLMDFEQ---LQPGDSVIQNASNSGVGQAVIQIAAALG 208

            AarViavdssed. pekklelAkelGAdldadfvnnskglptvnddrkedf
            +++ +v  ++d ++  + l+ +lG      a++v+      ++e
8Bpro    209 LRTINVVRDPDiQKLSDR LK-SLG---AEHVIT-----EEELR 243

            veaikeltgGrngagGvDvvl dcvGiglggatldaalallkpgGrlvvvG
            ++k +++      + +  +l+c      +gg++  ++l+ l++gG++v+ G
8Bpro    244 RPEMKNFFKDM---PQ PRLALNC---VGGKSSTELLRLQ LARGGTMV TYG 286

            pkvavGvpgggapipl..lllkeee klyersikGsflggrkprlsvlsvd
            G++  ++ +++ l++k      ++++G++l+++k  +
8Bpro    287 -----GMAKQPVASVs lLIFKD-----LKL RGFWLSQWKKD----- 318

            ttpdelreal dllasgikdkngkgvldplithtlpplddsleeaneAfel
            ++pd ++e++  l ++i+      +g+l      ++p l      + + A+e+
8Bpro    319 HSPDQFKELILTLC DLIR----RGQLTAPACSQVP-LQ----DYQSALEA 359

            lesgh.kkvvlip<-*
            ++  ++ k++l++
8Bpro    360 SMKPFIsSKQILTM      373

```

FIGURE 4